Remarks

I. The Amendments

The specification of the application was amended to add sequence identification numbers. Attached hereto as an Appendix is a marked-up version of the text showing the changes that were made.

The sequence listing submitted herewith corrects two errors that were made in the original sequence listing. Specifically, sequences 2 and 3 in the original sequence listing indicate that the first amino acid is valine whereas the presently submitted sequence listing indicates that the amino acid is methionine. The original error was the result of a glitch in the patent program used to generate the sequence. Specifically, the amino acid sequences of SEQ ID NO. 2 and SEQ ID NO. 3 were generated automatically by specifying the coding sequences of SEQ ID NO. 1. In particular, SEQ ID NO. 1 indicates that coding sequences occur at nucleotides 101-853 and at 853-1176. In both cases, the initial codon in the coding sequence is gtg. When this codon occurs within a coding sequence, its specifies the amino acid valine. However, when the codon is the first one in a coding sequence, it specifies the amino acid methionine. Unfortunately, the computer program used for generating the sequence listing originally filed does not recognize the distinction between a gtg sequence that occurs internally within a sequence listing, and a gtg sequence that occurs as the initial codon. Thus, sequences 2 and 3 in the sequence listing filed with the application begin with valine when they should, in fact, begin with methionine. Applicants submit that it is well known in the art of molecular biology and chemistry that proteins and encoded by genes ordinarily begin with methionine and that the codon gtg codes for methionine when it is at the start of a coding sequence. Applicants therefore submit that the amended sequences herein do not constitute new matter.

II. Submission of Computer Readable Form of Sequence Listing

Enclosed herewith is a 3.5 inch computer diskette containing a copy of the enclosed Sequence Listing in ASCII text.

III. Statements to Comply With Sequence Listing Rules

In compliance with 37 C.F.R. § 1.821(f), Applicants' undersigned attorney hereby states the content of the paper and computer readable copies of the Sequence Listing submitted herewith are the same. In accordance with 37 C.F.R. § 1.821(g), Applicants' undersigned attorney hereby states that the Sequence Listing submitted herewith does not add new matter to the application.

Conclusion

In light of the amendments and remarks above, Applicants submit that they have now fully complied with all Sequence Listing rules. It is therefore respectfully submitted that this application is now in condition for substantive review. If, in the opinion of the Examiner, a phone call may help to expedite the prosecution of this application, the Examiner is invited to call Applicants' undersigned attorney at (202) 419-7008.

Respectfully submitted,
FITCH, EVEN, TABIN & FLANNERY

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Appendix

Version with Markings to Show Changes Made

The specification has been amended herein to add sequence identification numbers. The changes that were made are shown below with the underlined words indicating text that was added.

On page 26, lines 16-19 to read as follows:

brnE, brnF, -forward:

5'-(AGC GCT GTC TGC TTA AGC CTT TTC)-3' (SEQ ID NO: 7)

brnE, brnF, -reverse:

5'-(GCG CGA TCA ATG GAA TCT AGC TTC)-3' (SEQ ID NO: 8)

On page 27 line 27 to page 28 line 2 to read as follows:

Universal primer:

5'-GTA AAA CGA CGG CCA GT-3' (SEQ ID NO: 9)

Reverse primer:

5'-GGA AAC AGC TAT GAC CAT G-3' (SEQ ID NO: 10)

On page 24 line 13 to page 25 line 12 to read as follows:

In order to clone the insertion site located downstream from transposon Tn5531 of the mutant described in Example 1.1, the chromosomal DNA of this mutant strain was first isolated as described in Schwarzer et al. (Bio/Technology (1990) 9: 84-87) and 400 ng thereof were cut with the restriction endonuclease EcoRI. The complete restriction batch was ligated into the vector pUC 18 (Norander et al., Gene (1983) 26: 101-106), likewise linearised with EcoRI, from Roche Diagnostics (Mannheim, Germany). The E. coli strain DH5amcr (Grant et al., Proceedings of the National Academy of Sciences of the United States of America (1990) 87: 4645-4649) was transformed with the

entire ligation batch by means of electroporation (Dower et al., Nucleic Acid Research (1988) 16: 6127-6145). Transformants in which the insertion sites of transposon Tn5531 were present in cloned form on the vector pUC 18 were identified by means of the carbenicillin and kanamycin resistance on LB agar plates containing 50 µg/mL of carbenicillin and 25 µg/mL of kanamycin. The plasmids were prepared from three of the transformants and the size of the cloned inserts determined by restriction analysis. The nucleotide sequence of the insertion site on one of the plasmids having an insert of a size of approx. 7.2 kb was determined using the dideoxy chain termination method of Sanger et al. (Proceedings of the National Academy of Sciences of the United States of America (1977) 74: 5463-5467). To this end, 1.3 kb of the insert were sequenced starting from the following oligonucleotide primer:

5'-CGG GTC TAC ACC GCT AGC CCA GG-3' (SEQ ID NO: 11)

On page 25 lines 13-25 to read as follows:

In order to identify the insertion site located upstream from the transposon, the chromosomal DNA of the mutants was cut with the restriction endonuclease PstI and ligated into vector pUC 18 which had been linearised with PstI. The remainder of the cloning operation was performed as described above. The nucleotide sequence of the insertion site on one of the plasmids having an insert of a size of approx. 4.8 kb was determined using the dideoxy chain termination method of Sanger et al. (Proceedings of the National Academy of Sciences of the United States of America (1977) 74: 5463-5467). To this end, 1.6 kb of the insert were sequenced starting from the following oligonucleotide primer: 5'-CGG TGC CTT ATC CAT TCA GG-3' (SEQ ID NO: 12)